

SEQUENCE LISTING

<110> Valenzuela et al.

<120> DORSAL TISSUE AFFECTING FACTOR AND COMPOSITIONS

<130> REG132-B1

<140> Not Yet Known

<141> Filed Herewith

<150> 09/167,874

<151> 1998-10-07

<150> 08/485,721

<151> 1995-07-06

<150> 08/392,935

<151> 1995-09-22

<150> PCT/US93/08326

<151> 1993-09-02

<150> 07/957,401

<151> 1992-10-06

<150> 07/950,410

<151> 1992-09-23

<150> 07/939,954

<151> 1992-09-03

<160> 22

<170> PatentIn Ver. 2.0

<210> 1

<211> 699

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(696)

<400> 1

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1				5				10					15			

gtc	ctg	ggg	ctg	cgg	gcg	aca	ccg	gcc	ggc	ggc	cag	cac	tat	ctc	cac	96
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Val Leu Gly Leu Arg Ala Thr Pro Ala Gly Gly Gln His Tyr Leu His
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atc cgc ccg gca ccc agc gac aac ctg ccc ctg gtg gac ctc atc gaa 144
 Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu
 35 40 45

cac cca gac cct atc ttt gac ccc aag gaa aag gat ctg aac gag acg 192
 His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr
 50 55 60

ctg ctg cgc tcg ctg ctc ggg ggc cac tac gac cca ggc ttc atg gcc 240
 Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala
 65 70 75 80

acc tcg ccc ccc gag gac cgg ccc ggc ggg ggc ggg ggt gca gct ggg 288
 Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Gly Ala Ala Gly
 85 90 95

ggc gcg gag gac ctg gcg gag ctg gac cag ctg ctg cgg cag cgg ccg 336
 Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro
 100 105 110

tcg ggg gcc atg ccg agc gag atc aaa ggg cta gag ttc tcc gag ggc 384
 Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly
 115 120 125

ttg gcc cag ggc aag aag cag cgc cta agc aag aag ctg cgg agg aag 432
 Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys
 130 135 140

tta cag atg tgg ctg tgg tcg cag aca ttc tgc ccc gtg ctg tac gcg 480
 Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr Ala
 145 150 155 160

tgg aac gac ctg ggc agc cgc ttt tgg ccg cgc tac gtg aag gtg ggc 528
 Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly
 165 170 175

agc tgc ttc agt aag cgc tcg tgc tcc gtg ccc gag ggc atg gtg tgc 576
 Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys
 180 185 190

aag ccg tcc aag tcc gtg cac ctc acg gtg ctg cgg tgg cgc tgt cag 624
 Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln
 195 200 205

cgg cgc ggg ggc cag cgc tgc ggc tgg att ccc atc cag tac ccc atc 672

Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile
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 Ile Ser Glu Cys Lys Cys Ser Cys
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Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu
 35 40 45

His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr
 50 55 60

Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala
 65 70 75 80

Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Gly Ala Ala Gly
 85 90 95

Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro
 100 105 110

Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly
 115 120 125

Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys
 130 135 140

Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr Ala
 145 150 155 160

Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly
 165 170 175

Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys

180

185

190

Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln
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Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile
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Ile Ser Glu Cys Lys Cys Ser Cys
 225 230

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09897322 070204
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Leu Arg Trp Arg Cys Gln Arg Arg

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Ile Ser Glu Cys Lys Cys Ser Cys

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:oligonucleotide

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<211> 37

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:oligonucleotide

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<210> 10

<211> 1180

<212> DNA

<213> mouse

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<222> (421)..(1116)

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 <222> (235)
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 tcgaaattaa cctcactaa agggaacaaa agctggagct ccaccgcggt ggcggccgcc 180
 ttcccaagta gagcggcggg ggggaattgc gaccaactcg tgcggtctt ctgcnccgcg 240
 gcgggagccg gcgctgcgcg aacggctctc ctgcagctc atgctgctg ccctgcgcct 300
 gctcagcctc gggtagcca cctccggagg gaccggggag cgcggcagcg ccgcggactc 360
 ggcgtgctct cctccgggga cgcgggacga agaggcagcc ccggggcgcg cgcgggaggc 420
 atg gag cgc tgc ccc agc ctg ggg gtc acc ctc tac gcc ctg gtg gtg 468
 Met Glu Arg Cys Pro Ser Leu Gly Val Thr Leu Tyr Ala Leu Val Val
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 gtc ctg ggg ctg cgg gca gca cca gcc ggc ggc cag cac tat cta cac 516
 Val Leu Gly Leu Arg Ala Ala Pro Ala Gly Gly Gln His Tyr Leu His
 20 25 30
 atc cgc cca gca ccc agc gac aac ctg ccc ttg gtg gac ctc atc gaa 564
 Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu
 35 40 45
 cat cca gac cct atc ttt gac cct aag gag aag gat ctg aac gag acg 612
 His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr
 50 55 60
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 Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala
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 Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Gly Pro Ala Gly
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ggt gcc gag gac ctg gcg gag ctg gac cag ctg ctg cgg cag cgg ccg 756
 Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro
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 Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly
 115 120 125

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 130 135 140

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 145 150 155 160

 tgg aat gac cta ggc agc cgc ttt tgg cca cgc tac gtg aag gtg ggc 948
 Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly
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 agc tgc ttc agc aag cgc tcc tgc tct gtg ccc gag ggc atg gtg tgt 996
 Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys
 180 185 190

 aag cca tcc aag tct gtg cac ctc acg gtg ctg cgg tgg cgc tgt cag 1044
 Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln
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 att tcc gag tgt aag tgt tcc tgc tagaactcgg gggggggcccc tgccccgcgcc 1146
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Val Leu Gly Leu Arg Ala Ala Pro Ala Gly Gly Gln His Tyr Leu His
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Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu
 35 40 45

His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr
 50 55 60

Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala
 65 70 75 80

Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Gly Pro Ala Gly
 85 90 95

Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro
 100 105 110

Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly
 115 120 125

Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys
 130 135 140

Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr Ala
 145 150 155 160

Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly
 165 170 175

Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys
 180 185 190

Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln
 195 200 205

Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile
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Ile Ser Glu Cys Lys Cys Ser Cys
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<210> 12

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100-443887-100

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<210> 17
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<212> DNA
<213> Artificial Sequence

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<400> 17

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<210> 18

<211> 18

<212> DNA

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<223> Description of Artificial Sequence:oligonucleotide

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<212> PRT

<213> mouse

<400> 19

Gln Met Trp Leu Trp Ser

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<210> 20

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:oligonucleotide

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gcaggaacac ttacactc

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<210> 21

<211> 6

<212> PRT

<213> mouse

<400> 21

Glu Cys Lys Cys Ser Cys

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<210> 22

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<223> Description of Artificial Sequence:oligonucleotide

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